



(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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MParch_n n.a. - n.a. database search, using Smith-Waterman algorithm
on: Thu Aug 21 10:35:24 1997; MasPar time 451.64 Seconds
929.139 Million cell updates/sec

Title: >US-08-469-637A-1
Description: (1-1527) from US08469637A.seq
Perfect Score: 1527 1 CGCCCGACCGCCGCTCCAA.....TTCACTGCAAAAAAAAAA 1527
N.A. Sequence: CGCGGTCGCGCGCGGAGGTT.....AAGTTGACCTTTTTTTTTT
Comp:

Scoring table:

TABLE default
Gap 6
Match STD : Dbase 0; Query 0

Searched: 359085 seqs, 137405154 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS-THREE
1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204
7:EST205 8:EST206 9:EST207 10:EST208 11:EST209 12:EST210
13:EST211 14:EST212 15:EST213 16:EST214 17:EST215
18:EST216 19:EST217 20:EST218 21:EST219 22:EST220
23:EST221 24:EST222 25:EST223 26:EST224 27:EST225
28:EST226 29:EST227 30:EST228 31:EST229 32:EST230
33:EST231 34:EST232 35:EST233 36:STS1 37:STS2 38:STS3
39:STS4 40:STS5 41:STS6 42:STS7 43:STS8 44:STS9 45:STS10
46:STS11 47:STS12 48:STS13
EST-STS-FOUR
49:EST51 50:EST52 51:EST53 52:EST54 53:EST55
54:EST56 55:EST57 56:EST58 57:EST59 58:EST60
59:EST61 60:EST62 61:EST63 62:EST64 63:EST65
64:EST66 65:EST67 66:EST68 67:EST69 68:EST70
69:EST71 70:EST72 71:EST73 72:EST74 73:EST75
74:EST76 75:EST77 76:EST78 77:EST79 78:EST80
79:EST81 80:EST82 81:EST83 82:EST84 83:EST85
84:EST86 85:EST87 86:EST88 87:EST89 88:EST90
89:EST91 90:EST92 91:EST93 92:EST94 93:EST95
94:EST96 95:EST97 96:EST98 97:EST99 98:EST100
99:EST101 100:EST102 101:EST103 102:EST104
103:EST105 104:EST106 105:EST107 106:EST108
107:EST109 108:EST110

Statistics: Mean 11.492; Variance 1.942; scale 5.918

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	461	30.2	463	65	AA233719	z447908.r1 Soares Nhh	0.00e+00
2	461	30.2	463	83	HS15151638	z447908.r1 Soares Nhh	0.00e+00
3	335	21.9	530	16	AA195113	z335a03.r1 Soares Nhh	0.00e+00
4	335	21.9	530	54	AA195113	z335a03.r1 Soares Nhh	0.00e+00
5	21	1.4	105	91	MM1135	mp53f02.r1 Soares 2nb	9.46e-03
6	21	1.4	107	98	MM117046	mp53f02.r1 Soares 2nb	9.46e-03
7	21	1.4	107	5	AA117046	mp53f02.r1 Soares 2nb	9.46e-03
8	21	1.4	156	36	DM36D7S	D. melanogaster STS d	9.46e-03
9	21	1.4	194	48	HUM075145	Human STS UT15145	9.46e-03
10	21	1.4	212	12	AA181616	z552d02.r1 Stratagene	9.46e-03
11	22	1.4	245	40	AT48713	15616 Arabidopsis tha	9.46e-03
12	21	1.4	253	38	G13923	human STS WT-13923	9.46e-03
13	21	1.4	253	38	G06067	human STS WT-6406	9.46e-03
14	22	1.4	267	95	MM5835	ms38f10.r1 Soares mou	9.47e-04
15	22	1.4	281	92	MM1157384	my25d08.r1 QuayWoodfo	9.47e-04
16	22	1.4	281	70	AA239461	my25d08.r1 QuayWoodfo	9.47e-04
17	22	1.4	312	42	G21574	human STS WT-13923	9.47e-04
18	22	1.4	343	59	AA124222	mp98c08.r1 Soares 2nb	9.47e-04
19	22	1.4	343	7	AA124222	mp98c08.r1 Soares 2nb	9.47e-04
20	22	1.4	343	99	MM1222422	mp98c08.r1 Soares 2nb	9.47e-04
21	21	1.4	351	36	DM122E4S	D. melanogaster STS d	9.46e-03
22	21	1.4	377	90	MM05110	mp83f02.r1 Soares 2nb	9.46e-03
23	21	1.4	380	60	AA142684	mp64e05.r1 Soares 2nb	9.46e-03
24	21	1.4	380	100	MM142684	mp64e05.r1 Soares 2nb	9.46e-03
25	21	1.4	392	33	T03759	mp64e05.r1 Soares 2nb	9.46e-03
26	22	1.4	400	39	G10922	18662 Infant Brain, B	9.47e-04
27	21	1.4	412	70	AA222925	human STS SHCC-13782	9.46e-03
28	21	1.4	422	67	AA241200	my98c06.r1 QuayWoodfo	9.46e-03
29	21	1.4	424	72	AA252560	my98c06.r1 Soares mou	9.46e-03
30	21	1.4	427	76	AT3618	z687h05.r1 Stratagene	9.46e-03
31	21	1.4	431	24	AA219045	z1139 Arabidopsis tha	9.46e-03
32	21	1.4	439	21	AA020160	z16f05.r1 Stratagene	9.46e-03
33	21	1.4	443	60	AA213094	my82b02.r1 Soares mou	9.46e-03
34	21	1.4	443	22	AA213094	my82b02.r1 Soares mou	9.46e-03
35	21	1.4	443	98	MM13451	my82b02.r1 Soares mou	9.46e-03
36	22	1.4	450	48	HUM071054	Human STS UT1054	9.47e-04
37	21	1.4	457	99	MM125146	mp78f05.r1 Soares 2nb	9.46e-03
38	21	1.4	457	60	AA125146	mp78f05.r1 Soares 2nb	9.46e-03
39	22	1.4	472	77	AT4774	5740 Arabidopsis tha	9.46e-03
40	22	1.4	496	75	AT35319	21953 Arabidopsis tha	9.46e-03
41	21	1.4	506	62	AA224501	z16f05.r1 Stratagene	9.46e-03
42	21	1.4	506	81	HS1144029	z16f05.r1 Stratagene	9.46e-03
43	21	1.4	589	22	MM12293	my40g03.r1 Soares 2nb	9.46e-03
44	21	1.4	589	22	AA210214	my40g03.r1 Soares 2nb	9.46e-03
45	21	1.4	1035	95	MM54110	mp68f10.r1 Soares mou	9.46e-03

ALIGNMENTS

RESULT 1
LOCUS AA233719 463 bp mRNA 28-FEB-1997
DEFINITION z447908.r1 Soares Nhhmpu SI Homo sapiens cDNA clone 665590 5'
ACCESSION AA233719
NID 91856711
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 463)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Eliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.

Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 448.

FEATURES

source

1..463

/organism="Homo sapiens"

/note="Organ: mixed (see below); Vector: p773D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBH, pregnant uterus
NbHPU, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

/clone="666590"

/tissue="Soares NbHMPU S1"

/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"

/lab_host="DH10B"

<1..>463

BASE COUNT

154 a 104 c 88 g 117 t

ORIGIN

MRNA

30.2%; Score 461; DB 65; Length 463;

Best Local Similarity 99.8%; Pred. No. 0.00e+00;

Matches 462; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match

1 aggcattgcaaacccagttgcaagatcctggaagctgctgagtttggcgataaataatg 60

995 AGGCATGCAAAACCCAGTGCAGATCCGTAAGCTGCTGAGTTGGCGATAAATAATG 1054

61 ggcgccaagaaaccttggaagggcctaagtgcagcctaagaacacacgtaaccct 120

1055 GCGACCAAGAACCTTGAAGGGCCTTAATGACGACATAAAGACATCAAGTACCT 1114

121 ttcccaaacctgtcactcagagctcctaagaagaccatcaggttccctcacagcttca 180

1115 TTCCCAAAACCTGTCACTAGAGTCTAAAGAACCATAGGTTCTTACAGCTTCAAAA 1174

181 tttcaaatgtatcagaagttatttttagaatagtatagtaaacaggttccaatcagtaa 240

1175 TGTCAAAATTTGTATACAGAAAGTTATTTAGAAATGATGATGATACCAAGGTCCAATCAGTAA 1234

241 aaataagctgttataactgaaatgagcattgagctgttccctcacacattggcgagatc 300

1235 AAATAAGCTGTTTAACTGGAATAATGGCCATTGAGCTGTTCCACAAATTTGGGAGATC 1294

301 ccattgagtgtaaacctgttctcagagcattgaggtcttcagtgatatactttctcat 360

1295 CCAATGATGATTAACCTGTTCTCAGGCACTTGAAGCTTTTAAAGTATCTTTTCTCATTTA 1354

361 ccagtgtaacttttggcacaggggtactaaagaataatgatgtggaagaaggactaac 420

1355 CCAAGTGAATTTTGGCACAGGGGTACTAAAGAAATCATGATGAGGAGAAAGGCTAAC 1414

421 atctccctcaataaaccacaaatggttaatccaactgtccagat 463

1415 ATCTCCTCAATAAACCCCAATGTTTATCCAACTGTCAAGAT 1457

RESULT

2

ID HS15151638 standard; RNA; EST; 463 BP.

AC AA233719;

NI g1856711

DT 06-MAR-1997 (Rel. 51, Created)

DT 06-MAR-1997 (Rel. 51, Last updated, Version 1)

DE z47908.r1 Soares NhMPU S1 Homo sapiens cDNA clone 666590 5'.

KW EST.

OS Homo sapiens (human)

OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

OC Vertebrata; Euthera; Primates; Catarrhini; Homnidae; Homo.

RN [1]

RP 1-463

RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,

RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,

RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,

RA Trevaskis E., Waterston R., Williamson A., Wohlmann P., Wilson R.,

RT "The WashU-Merck EST Project";

RL Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC estewatson.wustl.edu This clone is available royalty-free through

CC LNL; contact the IMAGE Consortium (infoimage.lnl.gov) for

CC further information. Seq primer: -28m13 rev2 ET from Amersham High

CC quality sequence stop: 448.

CC Key

Location/Qualifiers

1..463

/organism="Homo sapiens"

/note="Organ: mixed (see below); Vector: p773D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBH, pregnant uterus
NbHPU, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization reaction

The driver was PCR-amplified cDNAs from pools of 5,000

clones made from the same 3 libraries. The pools consisted

of I.M.A.G.E. clones 260232-265223, 340488-345479, and

484488-489479."

/clone="666590"

/tissue="Soares NhMPU S1"

/tissue_type="Pooled human melanocyte, fetal heart, and

pregnant uterus"

/lab_host="DH10B"

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Sequence 463 BP; 154 A; 104 C; 88 G; 117 T; 0 other;

Query Match

1 aggcattgcaaacccagttgcaagatcctggaagctgctgagtttggcgataaataatg 60

995 AGGCATGCAAAACCCAGTGCAGATCCGTAAGCTGCTGAGTTGGCGATAAATAATG 1054

61 ggcgccaagaaaccttggaagggcctaagtgcagcctaagaacacacgtaaccct 120

1055 GCGACCAAGAACCTTGAAGGGCCTTAATGACGACATAAAGACATCAAGTACCT 1114

121 ttcccaaacctgtcactcagagctcctaagaagaccatcaggttccctcacagcttca 180

1115 TTCCCAAAACCTGTCACTAGAGTCTAAAGAACCATAGGTTCTTACAGCTTCAAAA 1174

181 tttcaaatgtatcagaagttatttttagaatagtatagtaaacaggttccaatcagtaa 240

1175 TGTCAAAATTTGTATACAGAAAGTTATTTAGAAATGATGATGATACCAAGGTCCAATCAGTAA 1234

241 aaataagctgttataactgaaatgagcattgagctgttccctcacacattggcgagatc 300

1235 AAATAAGCTGTTTAACTGGAATAATGGCCATTGAGCTGTTCCACAAATTTGGGAGATC 1294

301 ccattgagtgtaaacctgttctcagagcattgaggtcttcagtgatatactttctcat 360

1295 CCAATGATGATTAACCTGTTCTCAGGCACTTGAAGCTTTTAAAGTATCTTTTCTCATTTA 1354

Db 361 ccagtgactatttccacagggactaaagaactatgatgtgagaaggaactaac 420
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QY 1355 CCACTGACTAATTTTGCACAGGGTACTAAAGAACTATGATGTGAGAGAGACTAAC 1414
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Db 421 atctccccaataaaccccaaatgttaatccaactctgagat 463
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QY 1415 ATCTCTCAATTAACCCCAATGTGTTAATCAACTGTCTGAGAT 1457
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RESULT 3 AA195113 530 bp mRNA EST 17-JAN-1997
LOCUS
DEFINITION zr35a03.r1 Soares Nhmpu S1 Homo sapiens CDNA clone 665356 5'.
ACCESSION AA195113
NID 91784803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 530)
REFERENCE
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
High quality sequence stop: 257.
Location/Qualifiers
FEATURES
source
1..530
/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT7/3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/clone_1lb="665356"
/clone_1lb="Soares Nhmpu S1"
/lab_host="DH10B"
BASE COUNT 170 a 96 c 93 g 168 t 3 others
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Query Match 21.9%; Score 335; DB 16; Length 530;
Best Local Similarity 97.7%; Pred. No. 0.00e+00;
Matches 342; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Db 1 acaaatgtatcagaagtatttttagaagaatgataagcagtcacatcaataaa 60
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QY 1178 ACAAAATGTATCAGAGTATTATTAGAAATGATAGTACCAAGTCCAAATCAATAAA 1237
|||||
Db 61 taagctcttaactgaatgagccattgagctgttccccaattggagatccca 120
|||||
QY 1238 TAACTGCTTAACTGGAATGCGCATGAGCTGTTCCACAAATGGCGAATCCCA 1297
|||||
Db 121 tgaatgaataacgtttctcaggcaacttgagcttcagtgatcatcttctcattaca 180
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QY 1298 TGGATGATGAATCTGTTTCTCAGGCACTTGAGGCTTCACTGATATCTTTCATTACCA 1357
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Db 181 gtgactaatttccacagggactaaagaactatgatgtgagaaggaactaac 240
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QY 1358 GTACTAATTTTCCACAGGGTACTAAAGAACTATGATGTGAGAGAGACTAACATC 1417
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Db 241 tctccaataaaccccaaatgttaatccaactgtcagatctgagatctatctagac 300
|||||
QY 1418 TCCTCAATTAACCCCAATGTGTTAATCAACTGTGATCTGATCTGATCTATCTATGAC 1477
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Db 301 tataattcccttactgctgtcgtaatttcgactggaataaaaa 350
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QY 1478 TATATTTTCCCTTATGCTGCTTGACGATATCACTGGAATAAAAAAAA 1527
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RESULT 4 AA195113 530 bp mRNA EST 14-FEB-1997
LOCUS
DEFINITION zr35a03.r1 Soares Nhmpu S1 Homo sapiens CDNA clone 665356 5'.
ACCESSION AA195113
NID 91784803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 530)
REFERENCE
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
High quality sequence stop: 257.
Location/Qualifiers
FEATURES
source
1..530
/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT7/3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/clone_1lb="665356"
/clone_1lb="Soares Nhmpu S1"
/issue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
BASE COUNT 170 a 96 c 93 g 168 t 3 others
ORIGIN
Query Match 21.9%; Score 335; DB 54; Length 530;
Best Local Similarity 97.7%; Pred. No. 0.00e+00;
Matches 342; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Db 1 acaaatgtatcagaagtatttttagaagaatgataagcagtcacatcaataaa 60
|||||

Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TGTTCGTAGTTCGTTGTTATTTGCA
Primer B: AAAGAGTCAGAAATGGGTTTTT
STS size: 100

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from random genomic sequence.

Location/Qualifiers

1..245

source /organism="Homo sapiens"

STS 56..155

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

primer_bind /map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

primer_bind complement(134..155)

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

BASE COUNT 92 a 28 c 35 g 87 t 3 others

ORIGIN

Query Match 1.4%; Score 21; DB 40; Length 245;

Best Local Similarity 70.8%; Pred. No. 9.46e-03;

Matches 34; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

109 tttctgaatgtaccctcattaaacacatttgactctttt 156

||||| ||||| ||||| ||||| ||||| ||||| |||||

519 TGCTTAGATGACGTCTCATTTGAGAAACCATCTGGACATCTTT 472

RESULT 13

LOCUS G06067 253 bp DNA 19-OCT-1995

DEFINITION human STS WI-6406.

ACCESSION G06067

NTD 9859312

KEYWORDS STS sequence; primer; sequence tagged site.

SOURCE human STS derived from sequences in dbEST and the Unigene

collection.

ORGANISM Homo sapiens

Eukaryota; Eukaryotes; Metazoa; Chordata;

Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;

Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;

Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 253)

AUTHORS Hudson, T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically

JOURNAL Mapped ESTs

COMMENT Unpublished (1995)

Contact: Thomas Hudson

Whitehead Institute/MIT Center for Genome Research

Whitehead Institute for Biomedical Research

9 Cambridge Center, Cambridge MA 02142 USA

Tel: 617 252 1900

Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu

Primer A: CATTCGTTTCATACATACATTC

Primer B: CACAGTGTGACAGCGTGC

STS size: 225

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from Z38433 -- dbEST.

Location/Qualifiers

1..253

source /organism="Homo sapiens"

STS 29..253

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

primer_bind /map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

primer_bind complement(235..253)

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

BASE COUNT 76 a 57 c 49 g 70 t 1 others

ORIGIN

Query Match 1.4%; Score 21; DB 38; Length 253;

Best Local Similarity 78.4%; Pred. No. 9.46e-03;

Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 123 aacagctcactgtcacgacataaactgtctcag 159

||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 774 ACACAGCTCACAGACAGACTTCCAGCTGCTGAAG 810

RESULT 14

ID MM5835 standard; RNA; EST; 267 BP.

AC W10583;

NI 91284900

DT 29-APR-1996 (Rel. 47, Created)

DR 03-MAR-1997 (Rel. 51, Last updated, Version 2)

DE ma38f10.r1 Soares mouse P3NMF19.5 Mus musculus cDNA clone 313003 5'

DE similar to gb:219554 VIMENTIN (HUMAN);.

KW EST.

OS Mus musculus (house mouse)

OC Eukaryota; Eukaryotes; Metazoa; Chordata;

OC Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

OC Mus.

RP 1-267

RA Warra M., Hillier L., Allen M., Bowles M., Dietrich N.,

RA Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,

RA Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,

RA Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,

RA Waterston R.,

